

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Applicant Name(s): THE GENE POOL, INC.
Street address: 300 Queen Anne Ave. N., Suite 392
City: Seattle
State/Province: Washington
Country: US
Postal code/Zip: 98109-4599
Phone number: (206) 526-8617 Fax number:

(ii) TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION

(iii) NUMBER OF SEQUENCES: 118

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Saliwanchik & Saliwanchik
(B) STREET: 2421 N.W. 41st St., Suite A-1
(C) CITY: Gainesville
(D) STATE: Florida
(E) COUNTRY: USA
(F) ZIP: 32606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bencen, Gerard H
(B) REGISTRATION NUMBER: 35,746
(C) REFERENCE/DOCKET NUMBER: GP-100.C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (904) 375-8100
(B) TELEFAX: (904) 372-5800

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

64

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGGATTCC CCA

13

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGGACTTT CCC

13

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGGGACTTT CCG

13

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

65

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGGGGACT TTCCA

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAGGGACT TTCCG

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGTTTTTC CCC

13

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGGACTTT CCGCTGGGGA CTTTCCA

27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGGGACTTT CCGCTGGGGA CTTTCCG

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

67

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTGGGGACT TTCCAGGGGA GGTGTG

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTGGGGACT TTCCGGGGAG CGTGGC

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGGGGACT TTCCGGGGAG GCGCGG

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

68

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCTGGGGACT TTCCAGAGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGGGGACT TTCCAGGGGA GCGGTG

26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

69

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTGGGGACT TTCCAGGGAG GCTGCC

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTCCAGGGA GCGGTGGCCT GGGCGGGACT GGG

33

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGTGGCCTGG GCGGGACTGG GGAGTGGCGT CCC

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCT

45

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGCAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCAT

45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGCGTG GCCT

44

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGGCGC GGCT

44

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGAGAGGCGT GGACT

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGCG TGGACT

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTACAGGGGA CTTTCCGCTG GGGACTTTC AGGGAGGCGT GGGGAG

46

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTACAGGGGA CTTTCCGCTG GGGACTTTC AGGGAGGCTG CCT

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTTCCGCTG GGGACTTTC AGGGAGGCGT GGCCTGGGCG GGACTGGG

48

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

74

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTCCAGGGA GGCCTGGCCT GGGCGGGACT GGGGAGTGGC GTCCC

45

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGG

59

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTCCGCTGG GGACTTTCCA GGGAGGCGTG GCCTGGGCGG GACTGGGGAG TGGCGTCCC

59

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTACAAGGGA CTTTCGCTG GGGACTTTC AGGGAGGCGT GGCCTGGGCG GGACTGGGGA 60
GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TATCACCGCC AGTGGTATTT ATGTCAACAC CGCCAGAGAT AATTTATCAC CGCAGATGGT 60
T 61

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TATCACCGCA AGGGATAAAT ATCTAACACC GTGCGTGTTG ACTATTTTAC CTCTGGCGGT 60
GATA 64

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGGA 60
GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGG 37

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGACTGGG GAGTGGCGTC CC

22

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGTAT CACCGCCAGT GGTATTTATG

60

TCAACACCGC CAGAGATAAT TTATCACCGC AGATGGTTCT GCA

103

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MÅ

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAACCATCTG CGGTGATAAA TTATCTCTGG CGGTGTTGAC ATAAATACCA CTGGCGGTGA

60

TA

62

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

78

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCCAACCA TCTGCGGTGA TAAATTATCT CTGGCGGTGT TGACATAAAT ACCACTGGCG 60
GTGATACTGC A 71

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATCACCGC CAGTGGTATT TATGTCAACA CCGCCAGAGA TAATTTATCA CCGCAGATGG 60
TTG 63

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCGGGGG GATACCCCC G 21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGGACTGGG GAGTGGCGTC CCTATCACCG CAAGGGATAA ATATCTAACA CCGTGC GTGT 60

TGACTATTTT ACCTCTGGCG GTGATAGCAT G 91

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAAGGGCGT AACCGAAATC GGTGTAACCG AAACCGGTTA GTATAAAGC AGA 53

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAGGGAGT AACCGAAAAC GGTCGGGACC GAAAACGGTG TATATAAAG ATGT 54

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTAGGGTGT AACCGAAAGC GGTTCACCG AAAACGGTGC ATATATAAAG CAAA

54

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTTCAACCG AATTCGGTTG CATG

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGCAACCG ATTCGGTTG CCTT

24

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TATGCAACCG AAATAGGTTG GGCA

24

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCCTAACCG TTTTCGGTTA CTTG

24

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGACTAACCG TTTTAGGTCA TATT

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GACGACTATC CAGCGACCAA GATCAGAGCC AGACACCGGA AACCCCTGCC AC

52

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GACGACACGG TATCCGCTAC TCAGCTTGTT AAACAGCTAC AGCACACCCC CTC

53

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GACGACGACC TGCAGACACC ACAGACACCG CCCAGCCCCT TACAAAGCTG TTCTGTGCAG

60

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CATACCAAAG CCGTCGCCTT GGGCACCGAA GAAACACAAC CACTAAGTTG TTGCACAGAG 60
ACTCAGTG 68

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TAATGTAATT GATTGTAATG ACTCTATGTG CAGTACCAGT ACCGTATTCC AGCACCGTGT 60
CCGTGGGCAC CGCAAAG 77

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAGACAACG ATAACCGACC ACCACAAGCA GCGGCCAAAC ACCCCGCCTT GGACAATAGA 60
ACAGCACGTA CTGCAACTAA 80

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATATGCAAT ACAATGCATT ATACAACTG GACACATATA TATATTTGTG AAGAAGCATC 60
AGTAACTGTG GTAGAGGGTC AAGTTGACTA TTATGGTTTA TATTATGTTC ATGAAGGAAT 120
ACGAACATAT TTTGTGCAGT TTAAAGATGA TGCAGAAAAA TATAGTAAAA ATAAAGTATG 180
GGAAGTTCAT GCGGGTGGTC AGGTAATATT ATGTCCTACA TCTGTGTTTA GCAGCAACGA 240
AGTATCCTCT CCTGAAATTA TTAGGC 266

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGGATGTATA AAAAAACATG GATATACAGT GGAAGTGCAG TTTGATGGAG ACATATGCTA 60
TTAGGCAGCA CTTGGCCAAC CACCCCGCCG CGACC 95

(2) INFORMATION FOR SEQ ID NO:62:

85

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CATGTTTTTT TATACATCCA TATCACCGCC AGTGGTATTT ATGTCAACAC CGCCAGAGAT 60
 AATTATCAC CGCAGATGGT T 81

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ala Asp Asp Asp Pro Tyr Gly Thr Gly Gln Met Phe His Leu Asn
 1 5 10 15
 Thr Ala Leu Thr His Ser Ile Phe Asn Ala Glu Leu Tyr Ser Pro Glu
 20 25 30
 Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu Glu Gln Pro
 35 40 45
 Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly Pro Ser His
 50 55 60
 Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys Ser Tyr Pro
 65 70 75 80
 Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val Ile Val Gln
 85 90 95
 Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His Ser Leu Val
 100 105 110

86

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | His | Cys | Glu | Asp | Gly | Val | Cys | Thr | Val | Thr | Ala | Gly | Pro | Lys | 115 | 120 | 125 |
| Asp | Met | Val | Val | Gly | Phe | Ala | Asn | Leu | Gly | Ile | Leu | His | Val | Thr | Lys | 130 | 135 | 140 |
| Lys | Lys | Val | Phe | Glu | Thr | Leu | Glu | Ala | Arg | Met | Thr | Glu | Ala | Cys | Ile | 145 | 150 | 155 |
| Arg | Gly | Tyr | Asn | Pro | Gly | Leu | Leu | Val | His | Ser | Asp | Leu | Ala | Tyr | Leu | 165 | 170 | 175 |
| Gln | Ala | Glu | Gly | Gly | Gly | Asp | Arg | Gln | Leu | Thr | Asp | Arg | Glu | Lys | Glu | 180 | 185 | 190 |
| Ile | Ile | Arg | Gln | Ala | Ala | Val | Gln | Gln | Thr | Lys | Glu | Met | Asp | Leu | Ser | 195 | 200 | 205 |
| Val | Val | Arg | Leu | Met | Phe | Thr | Ala | Phe | Leu | Pro | Asp | Ser | Thr | Gly | Ser | 210 | 215 | 220 |
| Phe | Thr | Arg | Arg | Leu | Glu | Pro | Val | Val | Ser | Asp | Ala | Ile | Tyr | Asp | Ser | 225 | 230 | 235 |
| Lys | Ala | Pro | Asn | Ala | Ser | Asn | Leu | Lys | Ile | Val | Arg | Met | Asp | Arg | Thr | 245 | 250 | 255 |
| Ala | Gly | Cys | Val | Thr | Gly | Gly | Glu | Glu | Ile | Tyr | Leu | Leu | Cys | Asp | Lys | 260 | 265 | 270 |
| Val | Gln | Lys | Asp | Asp | Ile | Gln | Ile | Arg | Phe | Tyr | Glu | Glu | Glu | Glu | Asn | 275 | 280 | 285 |
| Gly | Gly | Val | Trp | Glu | Gly | Phe | Gly | Asp | Phe | Ser | Pro | Thr | Asp | Val | His | 290 | 295 | 300 |
| Arg | Gln | Phe | Ala | Ile | Val | Phe | Lys | Thr | Pro | Lys | Tyr | Lys | Asp | Val | Asn | 305 | 310 | 315 |
| Ile | Thr | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Asp | Asp | Pro | Tyr | Leu | Gly | Arg | Pro | Glu | Gln | Met | Phe | His | 1 | 5 | 10 | 15 |
| Leu | Asp | Pro | Ser | Leu | Thr | His | Thr | Ile | Phe | Asn | Pro | Glu | Val | Phe | Gln | 20 | 25 | 30 | |
| Pro | Gln | Met | Ala | Leu | Pro | Thr | Ala | Asp | Gly | Pro | Tyr | Leu | Gln | Ile | Leu | 35 | 40 | 45 | |
| Glu | Gln | Pro | Lys | Gln | Arg | Gly | Phe | Arg | Phe | Arg | Tyr | Val | Cys | Glu | Gly | 50 | 55 | 60 | |
| Pro | Ser | His | Gly | Gly | Leu | Pro | Gly | Ala | Ser | Ser | Glu | Lys | Asn | Lys | Lys | 65 | 70 | 75 | 80 |
| Ser | Tyr | Pro | Gln | Val | Lys | Ile | Cys | Asn | Tyr | Val | Gly | Pro | Ala | Lys | Val | 85 | 90 | 95 | |
| Ile | Val | Gln | Leu | Val | Thr | Asn | Gly | Lys | Asn | Ile | His | Leu | His | Ala | His | 100 | 105 | 110 | |
| Ser | Leu | Val | Gly | Lys | His | Cys | Glu | Asp | Gly | Ile | Cys | Thr | Val | Thr | Ala | 115 | 120 | 125 | |
| Gly | Pro | Glu | Asp | Cys | Val | His | Gly | Phe | Ala | Asn | Leu | Gly | Ile | Leu | His | 130 | 135 | 140 | |
| Val | Thr | Lys | Lys | Lys | Val | Phe | Glu | Thr | Leu | Glu | Ala | Arg | Met | Thr | Glu | 145 | 150 | 155 | 160 |
| Ala | Cys | Ile | Arg | Gly | Tyr | Asn | Pro | Gly | Leu | Leu | Val | His | Pro | Asp | Leu | 165 | 170 | 175 | |
| Ala | Tyr | Leu | Gln | Ala | Glu | Gly | Gly | Gly | Asp | Arg | Gln | Leu | Gly | Asp | Arg | 180 | 185 | 190 | |
| Glu | Lys | Glu | Leu | Ile | Arg | Gln | Ala | Ala | Leu | Gln | Gln | Thr | Lys | Glu | Met | 195 | 200 | 205 | |
| Asp | Leu | Ser | Val | Val | Arg | Leu | Met | Phe | Thr | Ala | Phe | Leu | Pro | Asp | Ser | 210 | 215 | 220 | |
| Thr | Gly | Ser | Phe | Thr | Arg | Arg | Leu | Glu | Pro | Val | Val | Ser | Asp | Ala | Ile | 225 | 230 | 235 | 240 |
| Tyr | Asp | Ser | Lys | Ala | Pro | Asn | Ala | Ser | Asn | Leu | Lys | Ile | Val | Arg | Met | 245 | 250 | 255 | |
| Asp | Arg | Thr | Ala | Gly | Cys | Val | Thr | Gly | Gly | Glu | Glu | Ile | Tyr | Leu | Leu | 260 | 265 | 270 | |
| Cys | Asp | Lys | Val | Gln | Lys | Asp | Asp | Ile | Gln | Ile | Arg | Phe | Tyr | Glu | Glu | 275 | 280 | 285 | |

Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
 290 295 300

Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
 305 310 315 320

Asp Ile Asn Ile Thr
 325

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Glu Pro Ala Asp Leu Leu Pro Leu Tyr Leu Gln Pro Glu Trp Gly
 1 5 10 15

Glu Gln Glu Pro Gly Gly Ala Thr Pro Phe Val Glu Ile Leu Glu Gln
 20 25 30

Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser
 35 40 45

Ala Gly Ser Ile Pro Gly Glu His Ser Thr Asp Ser Ala Arg Thr His
 50 55 60

Pro Thr Ile Arg Val Asn His Tyr Arg Gly Pro Gly Arg Val Arg Val
 65 70 75 80

Ser Leu Val Thr Lys Asp Pro Pro His Gly Pro His Pro His Glu Leu
 85 90 95

Val Gly Arg His Cys Gln His Gly Tyr Tyr Glu Ala Glu Leu Ser Pro
 100 105 110

Asp Arg Ser Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys
 115 120 125

Lys Arg Glu Leu Glu Ala Ala Val Ala Glu Arg Ile Arg Thr Asn Asn
 130 135 140

Asn Pro Phe Asn Val Pro Met Glu Glu Arg Gly Ala Glu Tyr Asp Leu
 145 150 155 160

| Year | Month | Day | Hour | Minute | Second | Time | Location | Remarks |
|------|-------|-----|------|--------|--------|----------|----------|---------|
| 1900 | Jan | 1 | 10 | 10 | 10 | 10:10:10 | 1000 | 1000 |
| 1901 | Feb | 2 | 11 | 11 | 11 | 11:11:11 | 1100 | 1100 |
| 1902 | Mar | 3 | 12 | 12 | 12 | 12:12:12 | 1200 | 1200 |
| 1903 | Apr | 4 | 13 | 13 | 13 | 13:13:13 | 1300 | 1300 |
| 1904 | May | 5 | 14 | 14 | 14 | 14:14:14 | 1400 | 1400 |
| 1905 | Jun | 6 | 15 | 15 | 15 | 15:15:15 | 1500 | 1500 |
| 1906 | Jul | 7 | 16 | 16 | 16 | 16:16:16 | 1600 | 1600 |
| 1907 | Aug | 8 | 17 | 17 | 17 | 17:17:17 | 1700 | 1700 |
| 1908 | Sep | 9 | 18 | 18 | 18 | 18:18:18 | 1800 | 1800 |
| 1909 | Oct | 10 | 19 | 19 | 19 | 19:19:19 | 1900 | 1900 |
| 1910 | Nov | 11 | 20 | 20 | 20 | 20:20:20 | 2000 | 2000 |
| 1911 | Dec | 12 | 21 | 21 | 21 | 21:21:21 | 2100 | 2100 |
| 1912 | Jan | 13 | 22 | 22 | 22 | 22:22:22 | 2200 | 2200 |
| 1913 | Feb | 14 | 23 | 23 | 23 | 23:23:23 | 2300 | 2300 |
| 1914 | Mar | 15 | 24 | 24 | 24 | 24:24:24 | 2400 | 2400 |
| 1915 | Apr | 16 | 25 | 25 | 25 | 25:25:25 | 2500 | 2500 |
| 1916 | May | 17 | 26 | 26 | 26 | 26:26:26 | 2600 | 2600 |
| 1917 | Jun | 18 | 27 | 27 | 27 | 27:27:27 | 2700 | 2700 |
| 1918 | Jul | 19 | 28 | 28 | 28 | 28:28:28 | 2800 | 2800 |
| 1919 | Aug | 20 | 29 | 29 | 29 | 29:29:29 | 2900 | 2900 |
| 1920 | Sep | 21 | 30 | 30 | 30 | 30:30:30 | 3000 | 3000 |
| 1921 | Oct | 22 | 31 | 31 | 31 | 31:31:31 | 3100 | 3100 |
| 1922 | Nov | 23 | 32 | 32 | 32 | 32:32:32 | 3200 | 3200 |
| 1923 | Dec | 24 | 33 | 33 | 33 | 33:33:33 | 3300 | 3300 |
| 1924 | Jan | 25 | 34 | 34 | 34 | 34:34:34 | 3400 | 3400 |
| 1925 | Feb | 26 | 35 | 35 | 35 | 35:35:35 | 3500 | 3500 |
| 1926 | Mar | 27 | 36 | 36 | 36 | 36:36:36 | 3600 | 3600 |
| 1927 | Apr | 28 | 37 | 37 | 37 | 37:37:37 | 3700 | 3700 |
| 1928 | May | 29 | 38 | 38 | 38 | 38:38:38 | 3800 | 3800 |
| 1929 | Jun | 30 | 39 | 39 | 39 | 39:39:39 | 3900 | 3900 |
| 1930 | Jul | 31 | 40 | 40 | 40 | 40:40:40 | 4000 | 4000 |
| 1931 | Aug | 32 | 41 | 41 | 41 | 41:41:41 | 4100 | 4100 |
| 1932 | Sep | 33 | 42 | 42 | 42 | 42:42:42 | 4200 | 4200 |
| 1933 | Oct | 34 | 43 | 43 | 43 | 43:43:43 | 4300 | 4300 |
| 1934 | Nov | 35 | 44 | 44 | 44 | 44:44:44 | 4400 | 4400 |
| 1935 | Dec | 36 | 45 | 45 | 45 | 45:45:45 | 4500 | 4500 |
| 1936 | Jan | 37 | 46 | 46 | 46 | 46:46:46 | 4600 | 4600 |
| 1937 | Feb | 38 | 47 | 47 | 47 | 47:47:47 | 4700 | 4700 |
| 1938 | Mar | 39 | 48 | 48 | 48 | 48:48:48 | 4800 | 4800 |
| 1939 | Apr | 40 | 49 | 49 | 49 | 49:49:49 | 4900 | 4900 |
| 1940 | May | 41 | 50 | 50 | 50 | 50:50:50 | 5000 | 5000 |
| 1941 | Jun | 42 | 51 | 51 | 51 | 51:51:51 | 5100 | 5100 |
| 1942 | Jul | 43 | 52 | 52 | 52 | 52:52:52 | 5200 | 5200 |
| 1943 | Aug | 44 | 53 | 53 | 53 | 53:53:53 | 5300 | 5300 |
| 1944 | Sep | 45 | 54 | 54 | 54 | 54:54 | | |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asp | Leu | Phe | Pro | Leu | Ile | Phe | Pro | Ser | Glu | Pro | Ala | Gln | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Gly | Pro | Tyr | Val | Glu | Ile | Ile | Glu | Gln | Pro | Lys | Gln | Arg | Gly | Met |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Phe | Arg | Tyr | Lys | Cys | Glu | Gly | Arg | Ser | Ala | Gly | Ser | Ile | Pro | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Arg | Ser | Thr | Asp | Thr | Thr | Lys | Thr | His | Pro | Thr | Ile | Lys | Ile | Asn |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Tyr | Thr | Gly | Pro | Gly | Thr | Val | Arg | Ile | Ser | Leu | Val | Thr | Lys | Asp |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

(2) INFORMATION FOR SEQ ID NO:67:

(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) **HYPOTHETICAL: NO**

(v) FRAGMENT TYPE: internal

Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala
1 5 10 15

Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
 20 25 30
 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
 35 40 45
 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
 50 55 60
 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
 65 70 75 80
 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
 85 90 95
 Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
 100 105 110
 Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
 115 120 125
 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
 130 135 140
 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
 145 150 155 160
 Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
 165 170 175
 Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
 180 185 190
 Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
 195 200 205
 Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
 210 215 220
 Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
 225 230 235 240
 Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
 245 250 255
 Tyr Ala Asp Pro Ser Leu Gln
 260

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Pro | Asn | Gln | Asn | Asn | Gly | Ala | Ala | Pro | Gly | Gln | Gly | Pro | Ala | 1 | 5 | 10 | 15 |
| Val | Asp | Gly | Gln | Gln | Ser | Leu | Asn | Tyr | Asn | Gly | Leu | Pro | Ala | Gln | Gln | 20 | 25 | 30 | |
| Gln | Gln | Gln | Leu | Ala | Gln | Ser | Thr | Lys | Asn | Val | Arg | Lys | Lys | Pro | Tyr | 35 | 40 | 45 | |
| Val | Lys | Ile | Thr | Glu | Gln | Pro | Ala | Gly | Lys | Ala | Leu | Arg | Phe | Arg | Tyr | 50 | 55 | 60 | |
| Glu | Cys | Glu | Gly | Arg | Ser | Ala | Gly | Ser | Ile | Pro | Gly | Val | Asn | Ser | Thr | 65 | 70 | 75 | 80 |
| Pro | Glu | Asn | Lys | Thr | Tyr | Pro | Thr | Ile | Glu | Ile | Val | Gly | Tyr | Lys | Gly | 85 | 90 | 95 | |
| Arg | Ala | Val | Val | Val | Val | Ser | Cys | Val | Thr | Lys | Asp | Thr | Pro | Tyr | Arg | 100 | 105 | 110 | |
| Pro | His | Pro | His | Asn | Leu | Val | Gly | Lys | Glu | Gly | Cys | Lys | Lys | Gly | Val | 115 | 120 | 125 | |
| Cys | Thr | Leu | Glu | Ile | Asn | Ser | Glu | Thr | Met | Arg | Ala | Val | Phe | Ser | Asn | 130 | 135 | 140 | |
| Leu | Gly | Ile | Gln | Cys | Val | Lys | Lys | Lys | Asp | Ile | Glu | Ala | Ala | Leu | Lys | 145 | 150 | 155 | 160 |
| Ala | Arg | Glu | Glu | Ile | Arg | Val | Asp | Pro | Phe | Lys | Thr | Gly | Phe | Ser | His | 165 | 170 | 175 | |
| Arg | Phe | Gln | Pro | Ser | Ser | Ile | Asp | Leu | Asn | Ser | Val | Arg | Leu | Cys | Phe | 180 | 185 | 190 | |
| Gln | Val | Phe | Met | Glu | Ser | Glu | Gln | Lys | Gly | Arg | Phe | Thr | Ser | Pro | Leu | 195 | 200 | 205 | |
| Pro | Pro | Val | Val | Ser | Glu | Pro | Ile | Phe | Asp | Lys | Lys | Ala | Met | Ser | Asp | 210 | 215 | 220 | |
| Leu | Val | Ile | Cys | Arg | Leu | Cys | Ser | Cys | Ser | Ala | Thr | Val | Phe | Gly | Asn | 225 | 230 | 235 | 240 |
| Thr | Gln | Ile | Ile | Leu | Leu | Cys | Glu | Lys | Val | Ala | Lys | Glu | Asp | Ile | Ser | 245 | 250 | 255 | |

Val Arg Phe Phe Glu Glu Lys Asn Gly Gln Ser Val Trp Glu Ala Phe
 260 265 270

Gly Asp Phe Gln His Thr Asp Val His Lys Gln Thr Ala Ile Thr Phe
 275 280 285

Lys Thr Pro Arg Tyr His Thr Leu Asp Ile Thr
 290 295

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro
 1 5 10 15

Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Thr Arg Phe Arg
 20 25 30

Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser
 35 40 45

Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe
 50 55 60

Gly Lys Val Lys Ile Arg Thr Thr Leu Val Thr Lys Asn Glu Pro Tyr
 65 70 75 80

Lys Pro His Pro His Asp Leu Val Gly Lys Gly Cys Arg Asp Gly Tyr
 85 90 95

Tyr Glu Ala Glu Phe Gly Pro Glu Arg Gln Val Leu Ser Phe Gln Asn
 100 105 110

Leu Gly Ile Gln Cys Val Lys Lys Lys Asp Leu Lys Glu Ser Ile Ser
 115 120 125

Leu Arg Ile Ser Lys Lys Asn Pro Phe Asn Val Pro Glu Glu Gln Leu
 130 135 140

His Asn Ile Asp Glu Tyr Asp Leu Asn Val Val Arg Leu Cys Phe Gln
 145 150 155 160
 Ala Phe Leu Pro Asp Glu His Gly Asn Tyr Thr Leu Ala Leu Pro Pro
 165 170 175
 Leu Ile Ser Asn Pro Ile Tyr Asp Asn Arg Ala Pro Asn Thr Ala Glu
 180 185 190
 Leu Arg Ile Cys Arg Val Asn Lys Asn Cys Gly Ser Val Lys Gly Gly
 195 200 205
 Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Glu
 210 215 220
 Val Arg Phe Val Leu Gly Asn Trp Glu Ala Lys Gly Ser Phe Ser Gln
 225 230 235 240
 Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro Phe
 245 250 255
 Leu Gly Asp Ile Thr
 260

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro
 1 5 10 15
 Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Met Arg Phe Arg
 20 25 30
 Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser
 35 40 45
 Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe
 50 55 60
 Gly Lys Val Lys Ile Arg Thr Thr Leu Val Thr Lys Asn Glu Pro Tyr
 65 70 75 80

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--------|
| 1890 | 1891 | 1892 | 1893 | 1894 | 1895 | 1896 | 1897 | 1898 | 1899 | 1900 | 1901 | 1902 | 1903 | 1904 | 1905 | 1906 | 1907 | 1908 | 1909 | 1910 | 1911 | 1912 | 1913 | 1914 | 1915 | 1916 | 1917 | 1918 | 1919 | 1920 | 1921 | 1922 | 1923 | 1924 | 1925 | 1926 | 1927 | 1928 | 1929 | 1930 | 1931 | 1932 | 1933 | 1934 | 1935 | 1936 | 1937 | 1938 | 1939 | 1940 | 1941 | 1942 | 1943 | 1944 | 1945 | 1946 | 1947 | 1948 | 1949 | 1950 | 1951 | 1952 | 1953 | 1954 | 1955 | 1956 | 1957 | 1958 | 1959 | 1960 | 1961 | 1962 | 1963 | 1964 | 1965 | 1966 | 1967 | 1968 | 1969 | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | 2101 | 2102 | 2103 | 2104 | 2105 | 2106 | 2107 | 2108 | 2109 | 2110 | 2111 | 2112 | 2113 | 2114 | 2115 | 2116 | 2117 | 2118 | 2119 | 2120 | 2121 | 2122 | 2123 | 2124 | 2125 | 2126 | 2127 | 2128 | 2129 | 2130 | 2131 | 2132 | 2133 | 2134 | 2135 | 2136 | 2137 | 2138 | 2139 | 2140 | 2141 | 2142 | 2143 | 2144 | 2145 | 2146 | 2147 | 2148 | 2149 | 2150 | 2151 | 2152 | 2153 | 2154 | 2155 | 2156 | 2157 | 2158 | 2159 | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 | 2168 | 2169 | 2170 | 2171 | 2172 | 2173 | 2174 | 2175 | 2176 | 2177 | 2178 | 2179 | 2180 | 2181 | 2182 | 2183 | 2184 | 2185 | 2186 | 2187 | 2188 | 2189 | 2190 | 2191 | 2192 | 2193 | 2194 | 2195 | 2196 | 2197 | 2198 | 2199 | 2200 | 2201 | 2202 | 2203 | 2204 | 2205 | 2206 | 2207 | 2208 | 2209 | 2210 | 2211 | 2212 | 2213 | 2214 | 2215 | 2216 | 2217 | 2218 | 2219 | 2220 | 2221 | 2222 | 2223 | 2224 | 2225 | 2226 | 2227 | 2228 | 2229 | 2230 | 2231 | 2232 | 2233 | 2234 | 2235 | 2236 | 2237 | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | 2245 | 2246 | 2247 | 2248 | 2249 | 2250 | 2251 | 2252 | 2253 | 2254 | 2255 | 2256 | 2257 | 2258 | 2259 | 2260 | 2261 | 2262 | 2263 | 2264 | 2265 | 2266 | 2267 | 2268 | 2269 | 2270 | 2271 | 2272 | 2273 | 2274 | 2275 | 2276 | 2277 | 2278 | 2279 | 2280 | 2281 | 2282 | 2283 | 2284 | 2285 | 2286 | 2287 | 2288 | 2289 | 2290 | 2291 | 2292 | 2293 | 2294 | 2295 | 2296 | 2297 | 2298</ |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--------|

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
 20 25 30
 Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
 35 40 45
 Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
 50 55 60
 Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
 65 70 75 80
 Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
 85 90 95
 Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
 100 105 110
 Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
 115 120 125
 Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
 130 135 140
 Arg Ser His Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu Ser
 145 150 155 160
 His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr Glu
 165 170 175
 Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu Tyr
 180 185 190
 Asn Ser Gly Ser Glu Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly
 195 200 205
 Ser Asn Phe Leu Thr Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg
 210 215 220
 Val Val Asn Leu Glu Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg
 225 230 235 240
 Leu Thr Ala Ala Asn Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile
 245 250 255
 Asn Lys Phe Val Asn His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala
 260 265 270
 Ser Ile Tyr Thr Gln Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met
 275 280 285
 Phe Glu Ile Met Phe Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly
 290 295 300
 Arg Asp Leu Phe Glu Gln Leu Thr Ser Lys
 305 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys
1 5 10 15

Thr

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

Gly Asp Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys
1 5 10 15

Gly Lys Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp
20 25 30

His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys
35 40 45

Arg Phe Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr
50 55 60

Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg
65 70 75 80

[illegible]

| Ref | Author | Year | Country | Study Type | Findings |
|-----|----------|------|-------------|--------------|---|
| 1 | Smith | 1995 | USA | Case-control | Increased risk of lung cancer in smokers |
| 2 | Johnson | 1998 | UK | Cohort | Decreased risk of heart disease in vegetarians |
| 3 | Williams | 2001 | Canada | Case-control | Increased risk of breast cancer in women with history of miscarriage |
| 4 | Chen | 2003 | China | Cohort | Increased risk of liver cancer in people with chronic hepatitis B |
| 5 | Miller | 2005 | USA | Case-control | Increased risk of prostate cancer in men with family history |
| 6 | Lee | 2007 | South Korea | Cohort | Increased risk of stomach cancer in people with H. pylori infection |
| 7 | Wong | 2009 | Hong Kong | Case-control | Increased risk of colorectal cancer in people with inflammatory bowel disease |
| 8 | Nguyen | 2011 | Vietnam | Cohort | Increased risk of liver cancer in people with chronic hepatitis B |
| 9 | Patel | 2013 | India | Case-control | Increased risk of breast cancer in women with history of miscarriage |
| 10 | Kim | 2015 | South Korea | Cohort | Increased risk of stomach cancer in people with H. pylori infection |
| 11 | Alam | 2017 | Bangladesh | Case-control | Increased risk of liver cancer in people with chronic hepatitis B |
| 12 | Yamamoto | 2019 | Japan | Cohort | Increased risk of stomach cancer in people with H. pylori infection |
| 13 | Abdullah | 2021 | Malaysia | Case-control | Increased risk of breast cancer in women with history of miscarriage |
| 14 | Chen | 2022 | China | Cohort | Increased risk of liver cancer in people with chronic hepatitis B |
| 15 | Smith | 2023 | USA | Case-control | Increased risk of prostate cancer in men with family history |

| Author | Year | Country | Study |
|-----------|------|-----------|----------|
| 1. Smith | 1995 | USA | Study 1 |
| 2. Jones | 1998 | UK | Study 2 |
| 3. Brown | 2001 | Canada | Study 3 |
| 4. White | 2003 | Australia | Study 4 |
| 5. Black | 2005 | Germany | Study 5 |
| 6. Green | 2007 | France | Study 6 |
| 7. Grey | 2009 | Italy | Study 7 |
| 8. White | 2011 | Spain | Study 8 |
| 9. Black | 2013 | Japan | Study 9 |
| 10. Brown | 2015 | India | Study 10 |

- | Year | Revenue | Expenditure | Surplus |
|--------|---------|-------------|---------|
| 1911 | 100 | 100 | 0 |
| 1912 | 100 | 100 | 0 |
| 1913 | 100 | 100 | 0 |
| 1914 | 100 | 100 | 0 |
| 1915 | 100 | 100 | 0 |
| 1916 | 100 | 100 | 0 |
| 1917 | 100 | 100 | 0 |
| 1918 | 100 | 100 | 0 |
| 1919 | 100 | 100 | 0 |
| 1920 | 100 | 100 | 0 |
| 1921 | 100 | 100 | 0 |
| 1922 | 100 | 100 | 0 |
| 1923 | 100 | 100 | 0 |
| 1924 | 100 | 100 | 0 |
| 1925 | 100 | 100 | 0 |
| 1926 | 100 | 100 | 0 |
| 1927 | 100 | 100 | 0 |
| 1928 | 100 | 100 | 0 |
| 1929 | 100 | 100 | 0 |
| 1930 | 100 | 100 | 0 |
| 1931 | 100 | 100 | 0 |
| 1932 | 100 | 100 | 0 |
| 1933 | 100 | 100 | 0 |
| 1934 | 100 | 100 | 0 |
| 1935 | 100 | 100 | 0 |
| 1936 | 100 | 100 | 0 |
| 1937 | 100 | 100 | 0 |
| 1938 | 100 | 100 | 0 |
| 1939 | 100 | 100 | 0 |
| 1940 | 100 | 100 | 0 |
| 1941 | 100 | 100 | 0 |
| 1942 | 100 | 100 | 0 |
| 1943 | 100 | 100 | 0 |
| 1944 | 100 | 100 | 0 |
| 1945 | 100 | 100 | 0 |
| 1946 | 100 | 100 | 0 |
| 1947 | 100 | 100 | 0 |
| 1948 | 100 | 100 | 0 |
| 1949 | 100 | 100 | 0 |
| 1950 | 100 | 100 | 0 |
| 1951 | 100 | 100 | 0 |
| 1952 | 100 | 100 | 0 |
| 1953 | 100 | 100 | 0 |
| 1954 | 100 | 100 | 0 |
| 1955 | 100 | 100 | 0 |
| 1956 | 100 | 100 | 0 |
| 1957 | 100 | 100 | 0 |
| 1958 | 100 | 100 | 0 |
| 1959 | 100 | 100 | 0 |
| 1960 | 100 | 100 | 0 |
| 1961 | 100 | 100 | 0 |
| 1962 | 100 | 100 | 0 |
| 1963 | 100 | 100 | 0 |
| 1964 | 100 | 100 | 0 |
| 1965 | 100 | 100 | 0 |
| 1966 | 100 | 100 | 0 |
| 1967 | 100 | 100 | 0 |
| 1968 | 100 | 100 | 0 |
| 1969 | 100 | 100 | 0 |
| 1970 | 100 | 100 | 0 |
| 1971 | 100 | 100 | 0 |
| 1972 | 100 | 100 | 0 |
| 1973 | 100 | 100 | 0 |
| 1974 | 100 | 100 | 0 |
| 1975 | 100 | 100 | 0 |
| 1976 | 100 | 100 | 0 |
| 1977 | 100 | 100 | 0 |
| 1978 | 100 | 100 | 0 |
| 1979 | 100 | 100 | 0 |
| 1980 | 100 | 100 | 0 |
| 1981 | 100 | 100 | 0 |
| 1982 | 100 | 100 | 0 |
| 1983 | 100 | 100 | 0 |
| 1984 | 100 | 100 | 0 |
| 1985 | 100 | 100 | 0 |
| 1986 | 100 | 100 | 0 |
| 1987 | 100 | 100 | 0 |
| 1988 | 100 | 100 | 0 |
| 1989 | 100 | 100 | 0 |
| 1990 | 100 | 100 | 0 |
| 1991 | 100 | 100 | 0 |
| 1992 | 100 | 100 | 0 |
| 1993 | 100 | 100 | 0 |
| 1994 | 100 | 100 | 0 |
| 1995 | 100 | 100 | 0 |
| 1996 | 100 | 100 | 0 |
| 1997 | 100 | 100 | 0 |
| 1998 | 100 | 100 | 0 |
| 1999 | 100 | 100 | 0 |
| 2000 | 100 | 100 | 0 |
| 2001 | 100 | 100 | 0 |
| 2002 | 100 | 100 | 0 |
| 2003 | 100 | 100 | 0 |
| 2004 | 100 | 100 | 0 |
| 2005 | 100 | 100 | 0 |
| 2006 | 100 | 100 | 0 |
| 2007</ | | | |

1998

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ile | Val | Pro | Gln | Leu | Gln | Asn | Ile | Val | Ser | Thr | Val | Asn | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Cys | Lys | Leu | Asp | Leu | Lys | Thr | Ile | Ala | Leu | Arg | Ala | Arg | Asn | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Tyr | Asn | Pro | Lys | Arg | Phe | Ala | Ala | Val | Ile | Met | Arg | Ile | Arg | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Arg | Thr | Thr | Ala | Leu | Ile | Phe | Ser | Ser | Gly | Lys | Met | Val | Cys | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Ala | Lys | Ser | Glu | Glu | Gln | Ser | Arg | Leu | Ala | Ala | Arg | Lys | Tyr | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Arg | Val | Val | Gln | Lys | Leu | Gly | Phe | Pro | Ala | Lys | Phe | Leu | Asp | Phe | Lys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ile | Gln | Asn | Met | Val | Gly | Ser | Cys | Asp | Val | Lys | Phe | Pro | Ile | Arg | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Glu Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu
 115 120 125
 Leu Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu
 130 135 140
 Leu Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg
 145 150 155 160
 Ala Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly
 165 170 175
 Phe Arg Lys Thr Thr
 180

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln Val Lys Cys Tyr
 1 5 10 15
 Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr Glu Asn Cys Thr
 20 25 30
 Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu Arg Gln Gly Gln
 35 40 45
 Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln Arg Gln Asp Phe
 50 55 60
 Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile Ser Gly Phe Thr
 65 70 75 80
 Ala Ser Leu Asp Phe
 85

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

100

(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Cys Pro Cys Leu Leu Ile Gly Thr Ser Gly Asn Gly Asn Gln Val Lys
1 5 10 15

Cys Tyr Ser Phe Arg Val Lys Arg Trp His Asp Arg Asp Lys Tyr His
20 25 30

His Thr Thr Thr Trp Trp Ala Val Gly Gly Gln Gly Ser Glu Arg Pro
35 40 45

Gly Asp Ala Thr Val Ile Val Thr Phe Lys Asp Gln Ser Gln Arg Ser
50 55 60

His Phe Leu Gln Gln Val Pro Leu Pro Pro Gly Met Ser Ala His Gly
65 70 75 80

Val Thr Met Thr Val Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Pro Pro Val Ile Cys Leu Lys Gly Gly His Asn Gln Leu Lys Cys Leu
1 5 10 15

Arg Tyr Arg Leu Lys Ser Lys His Ser Ser Leu Phe Asp Cys Ile Ser
20 25 30

101

Thr Thr Trp Ser Trp Val Asp Thr Thr Ser Thr Cys Arg Leu Gly Ser
 35 40 45

Gly Arg Met Leu Ile Lys Phe Ala Asp Ser Glu Gln Arg Asp Lys Phe
 50 55 60

Leu Ser Arg Val Pro Leu Pro Ser Thr Thr Gln Val Phe Leu Gly Asn
 65 70 75 80

Phe Tyr Gly Leu

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Pro Val Ile Leu Val Arg Gly Gly Ala Asn Thr Leu Lys Cys Phe
 1 5 10 15

Arg Asn Arg Ala Arg Val Arg Tyr Arg Gly Leu Phe Lys Tyr Phe Ser
 20 25 30

Thr Thr Trp Ser Trp Val Ala Gly Asp Ser Thr Glu Arg Leu Gly Arg
 35 40 45

Ser Arg Met Leu Ile Leu Phe Thr Ser Ala Cys Gln Arg Glu Lys Pro
 50 55 60

Asp Glu Thr Val Lys Tyr Pro Lys Gly Val Asp Thr Ser Tyr Gly Asn
 65 70 75 80

Leu Asp Ser Leu

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Val | Val | Cys | Val | Lys | Gly | Gly | Ala | Asn | Gln | Leu | Lys | Cys | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Tyr | Arg | Leu | Lys | Ala | Ser | Thr | Gln | Val | Asp | Phe | Asp | Ser | Ile | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Thr | Trp | His | Trp | Thr | Asp | Arg | Lys | Asn | Thr | Glu | Arg | Ile | Gly | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Arg | Met | Leu | Val | Lys | Phe | Ile | Asp | Glu | Ala | Gln | Arg | Glu | Lys | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Glu | Arg | Val | Ala | Leu | Pro | Arg | Ser | Val | Ser | Val | Phe | Leu | Gly | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Phe | Asn | Gly | Ser | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Ile | Val | Gln | Leu | Gln | Gly | Asp | Ser | Asn | Cys | Leu | Lys | Cys | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Tyr | Arg | Leu | Asn | Asp | Lys | Tyr | Lys | His | Leu | Phe | Glu | Leu | Ala | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Thr | Trp | His | Trp | Ala | Ser | Pro | Glu | Ala | Pro | His | Lys | Asn | Ala | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Thr | Leu | Thr | Tyr | Ser | Ser | Glu | Glu | Gln | Arg | Gln | Gln | Phe | Leu | Asn |
| | 50 | | | | | 55 | | | | | | 60 | | | |

Ser Val Lys Ile Pro Pro Thr Ile Arg His Lys Val Gly Phe Met Ser
 65 70 75 80

Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Pro Ile Val Gln Phe Gln Gly Glu Ser Asn Cys Leu Lys Cys Phe
 1 5 10 15

Arg Tyr Arg Leu Asn Arg Asp His Arg His Leu Phe Asp Leu Ile Ser
 20 25 30

Ser Thr Trp His Trp Ala Ser Ser Lys Ala Pro His Lys His Ala Ile
 35 40 45

Val Thr Val Thr Tyr Asp Ser Glu Glu Gln Arg Gln Gln Phe Leu Asp
 50 55 60

Val Val Lys Ile Pro Pro Thr Ile Ser His Lys Leu Gly Phe Met Ser
 65 70 75 80

Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

104

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Ile | Ile | His | Leu | Lys | Gly | Asp | Arg | Asn | Ser | Leu | Lys | Cys | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Tyr | Arg | Leu | Arg | Lys | His | Ser | Asp | His | Tyr | Arg | Asp | Ile | Ser | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Trp | His | Trp | Thr | Gly | Ala | Gly | Asn | Glu | Lys | Thr | Gly | Ile | Leu | Thr |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Val | Thr | Tyr | His | Ser | Glu | Thr | Gln | Arg | Thr | Lys | Phe | Leu | Asn | Thr | Val |
| | | | 50 | | | | 55 | | | | 60 | | | | |
| Ala | Ile | Pro | Asp | Ser | Val | Gln | Ile | Leu | Val | Gly | Tyr | Asn | Thr | Met | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Ile | Val | His | Leu | Lys | Gly | Asp | Ala | Asn | Thr | Leu | Lys | Cys | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Tyr | Arg | Phe | Lys | Lys | His | Cys | Thr | Leu | Tyr | Thr | Ala | Val | Ser | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Trp | His | Trp | Thr | Gly | His | Asn | Tyr | Lys | His | Lys | Ser | Ala | Ile | Val |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Thr | Leu | Thr | Tyr | Asp | Ser | Glu | Trp | Gln | Arg | Asp | Gln | Phe | Leu | Ser | Gln |
| | | | 50 | | | | 55 | | | | 60 | | | | |
| Val | Lys | Ile | Pro | Lys | Thr | Ile | Thr | Val | Ser | Thr | Gly | Phe | Met | Ser | Ile |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

105

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Ala | Pro | Ile | Val | His | Leu | Lys | Gly | Glu | Ser | Asn | Ser | Leu | Lys | Cys | Leu | 1 | 5 | 10 | 15 |
| Arg | Tyr | Arg | Leu | Lys | Pro | Tyr | Asn | Glu | Leu | Tyr | Ser | Ser | Met | Ser | Ser | 20 | 25 | 30 | |
| Thr | Trp | His | Trp | Thr | Ser | Asp | Asn | Lys | Asn | Ser | Lys | Asn | Gly | Ile | Val | 35 | 40 | 45 | |
| Thr | Val | Thr | Phe | Val | Thr | Gly | Gln | Gln | Gln | Gln | Met | Phe | Leu | Gly | Thr | 50 | 55 | 60 | |
| Val | Lys | Ile | Pro | Pro | Thr | Val | Gln | Ile | Ser | Thr | Gly | Phe | Met | Thr | Leu | 65 | 70 | 75 | 80 |
| Val | | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|---|----|----|
| Gly | Ile | Val | Glu | Gln | Cys | Cys | Thr | Ser | Ile | Cys | Ser | Leu | Tyr | Gln | Leu | 1 | 5 | 10 | 15 |
| Glu | Asn | Tyr | Cys | Asn | | | | | | | | | | | | 20 | | | |

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Val | Asn | Gln | His | Leu | Cys | Gly | Ser | His | Leu | Val | Glu | Ala | Leu | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Cys | Gly | Glu | Arg | Gly | Phe | Phe | Tyr | Thr | Pro | Lys | Thr |
| | | | 20 | | | | | 25 | | | | | 30 |

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Val | Glu | Gln | Cys | Cys | Ala | Ser | Val | Cys | Ser | Leu | Tyr | Gln | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | |
|-----|-----|-----|-----|-----|
| Glu | Asn | Tyr | Cys | Asn |
| | | | 20 | |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Ile
1 5 10 15

Lys Arg Ser Leu Ala Arg Phe Cys
20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

108

Asp Ser Trp Met Glu Glu Val Ile Lys Ile Cys Gly Arg Glu Leu Val
 1 5 10 15

Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Ser
 20 25 30

Leu

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu Glu Lys Met Gly Thr Ala Lys Lys Cys Cys Ala Ile Gly Cys Ser
 1 5 10 15

Thr Glu Asp Phe Arg Met Val Cys
 20

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Arg Pro Asn Trp Glu Glu Arg Ser Arg Leu Cys Gly Arg Asp Leu Ile
 1 5 10 15

Arg Ala Phe Ile Tyr Leu Cys Gly Gly Thr Arg Trp Thr Arg Leu Pro
 20 25 30

Asn Phe Gly Asn Tyr Pro Ile Met
35 40

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Gly Ile Val Pro Thr Leu Gln Asn Ile Val Ser Thr Val Asn Leu
1 5 10 15

Asp Cys Lys Leu Asp Leu Lys Ala Ile Ala Leu Gln Ala Arg Asn Ala
20 25 30

Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu
35 40 45

Pro Lys Thr Thr Ala Leu Ile Phe Ala Ser Gly Lys Met Val Cys Thr
50 55 60

Gly Ala Lys Ser Glu Asp Phe Ser Lys Met Ala Ala Arg Lys Tyr Ala
65 70 75 80

Arg Ile Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Lys Asp Phe Lys
85 90 95

Ile Gln Asn Ile Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu
100 105 110

Glu Gly Leu Ala Tyr Ser His Ala Ala Phe Ser Ser Tyr Glu Pro Glu
115 120 125

Leu Phe Pro Gly Leu Ile Tyr Arg Met Lys Val Pro Lys Ile Val Leu
130 135 140

Leu Ile Phe Val Ser Gly Lys Ile Val Ile Thr Gly Ala Lys Met Arg
145 150 155 160

Asp Glu Thr Tyr Lys Ala Phe Glu Asn Ile Tyr Pro Val Leu Ser Glu
165 170 175

Phe Arg Lys Ile Gln Gln
180

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asn Ser Asn Ser Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
20 25 30

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
35 40 45

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
50 55 60

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
65 70 75 80

Phe Met Ser Ile

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
1 5 10 15

111

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
 20 25 30
 Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
 35 40 45
 Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
 50 55 60
 Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
 65 70 75 80
 Phe Met Ser Ile

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ser Gly Asn Thr Thr Pro Ile Ile His Leu Lys Gly Asp Arg Asn Ser
 1 5 10 15
 Leu Lys Cys Leu Arg Tyr Arg Leu Arg Lys His Ser Asp His Tyr Arg
 20 25 30
 Asp Ile Ser Ser Thr Trp His Trp Thr Gly Ala Gly Asn Glu Lys Thr
 35 40 45
 Gly Ile Leu Thr Val Thr Tyr His Ser Glu Thr Gln Arg Thr Lys Phe
 50 55 60
 Leu Asn Thr Val Ala Ile Pro Asp Ser Val Gln Ile Leu Val Gly Tyr
 65 70 75 80
 Met Thr Met

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid

112

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Gly Asn Thr Ala Pro Ile Val His Leu Lys Gly Glu Ser Asn Ser
1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Leu Lys Pro Tyr Lys Glu Leu Tyr Ser
20 25 30

Ser Met Ser Ser Thr Trp His Trp Thr Ser Asp Asn Lys Asn Ser Lys
35 40 45

Asn Gly Ile Val Thr Val Thr Phe Val Thr Glu Gln Gln Gln Gln Met
50 55 60

Phe Leu Gly Thr Val Lys Ile Pro Pro Thr Val Gln Ile Ser Thr Gly
65 70 75 80

Phe Met Thr Leu

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Gly Asn Thr Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln
1 5 10 15

Val Lys Cys Tyr Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr
20 25 30

Glu Asn Cys Thr Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu
35 40 45

Arg Gln Gly Gln Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln
50 55 60

Arg Gln Asp Phe Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile
65 70 75 80

Ser Gly Phe Thr Ala Ser Leu Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ser Asn Lys Lys Thr Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asn Ser Asn Thr
1

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids

114

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Gly Asn Thr
1

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Ser Ser Gly Ser Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Cys Tyr Pro Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Glu Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
50 55 60

Thr Ala
65

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

116

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60
 Thr Ala
 65

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 1 5 10 15
 Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60
 Thr Ala
 65

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

117

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Ser Thr Lys Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala Arg
 1              5              10              15
Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu Ser
      20              25              30
Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val Gly
      35              40              45
Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala Leu
      50              55              60
Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile
      65              70              75              80
Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Glu Pro Ser
      85              90              95

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Ser Thr Lys Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala Arg
 1              5              10              15
Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu Ser
      20              25              30
Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val Gly
      35              40              45
Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala Leu
      50              55              60
Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile
      65              70              75              80

```

Ala Arg Glu Ile Tyr Glu Met Cys Glu Ala Val Ser Met Glu Pro Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp
20 25 30

Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val
35 40 45

Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe
50 55 60

Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro
65 70 75 80

Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala
85 90 95

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
100 105 110

Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
115 120 125

Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
130 135 140

Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
145 150 155 160

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
165 170 175

Phe Met Ser Ile
180

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
 1 5 10 15
 Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp
 20 25 30
 Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val
 35 40 45
 Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe
 50 55 60
 Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro
 65 70 75 80
 Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala
 85 90 95
 Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys
 100 105 110
 Thr

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15
Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser
20 25 30
Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
35 40 45
Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
50 55 60
Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
65 70 75 80
Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
85 90 95
Thr Ala Ser Asn Lys Lys Thr Thr Ala Ser Ser Gly Ser Ser Gly Ser
100 105 110
Gly Ile Val Pro Gln Leu Gln Asn Ile Val Ser Thr Val Asn Leu Gly
115 120 125
Cys Lys Leu Asp Leu Lys Thr Ile Ala Leu Arg Ala Arg Asn Ala Glu
130 135 140
Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu Pro
145 150 155 160
Arg Thr Thr Ala Leu Ile Phe Ser Ser Gly Lys Met Val Cys Thr Gly
165 170 175
Ala Lys Ser Glu Glu Gln Ser Arg Leu Ala Ala Arg Lys Tyr Ala Arg
180 185 190
Val Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Leu Asp Phe Lys Ile
195 200 205
Gln Asn Met Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu Glu
210 215 220
Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu Leu
225 230 235 240
Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu Leu
245 250 255
Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg Ala
260 265 270
Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly Phe
275 280 285

Arg Lys Thr Thr
290

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser
20 25 30

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
35 40 45

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
50 55 60

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
65 70 75 80

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
85 90 95

Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys
100 105 110

Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr
115 120 125

Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe
130 135 140

Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu
145 150 155 160

Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys
165 170 175

Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His
180 185 190

122

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Thr | His | Gln | Asn | Lys | Lys | Gly | Gly | Pro | Gly | Val | Ala | Leu | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Val | Gly | Thr | Leu | Pro | Leu | Asp | Ser | Gly | Ala | Gly | Ser | Glu | Gly | Ser | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Ala | Thr | Pro | Ser | Ala | Leu | Ile | Thr | Thr | Asn | Met | Val | Ala | Met | Glu |
| | 225 | | | | | 230 | | | | 235 | | | | | 240 |
| Ala | Ile | Cys | Pro | Glu | Gly | Ile | Ala | Arg | Leu | Ala | Asn | Ser | Gly | Ile | Asn |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Val | Met | Gln | Val | Ala | Asp | Leu | Gln | Ser | Ile | Asn | Ile | Ser | Gly | Asn | Gly |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Phe | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Tyr | Ser | Ala | Leu | Ala | Asn | Lys | Cys | Cys | His | Val | Gly | Cys | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Arg | Ser | Leu | Ala | Arg | Phe | Cys | Met | Ser | Met | Arg | Gln | Arg | Ile | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Lys | Asp | Tyr | Ala | Met | Arg | Phe | Gly | Gln | Thr | Lys | Thr | Ala | Lys | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Gly | Val | Tyr | Gln | Ser | Ala | Ile | Asn | Lys | Ala | Ile | His | Ala | Gly | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Ile | Phe | Leu | Thr | Ile | Asn | Ala | Asp | Gly | Ser | Val | Tyr | Ala | Glu | Glu |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Val | Lys | Pro | Phe | Pro | Ser | Asn | Lys | Lys | Thr | Thr | Ala | Ser | Asn | Lys | Lys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Thr | Ala | Met | Ala | Asp | Asp | Asp | Pro | Tyr | Gly | Thr | Gly | Gln | Met | Phe |
| | | | 100 | | | | | 105 | | | | | 110 | | |

123

| | | |
|---------|---|-------------------------------------|
| His Leu | Asn Thr Ala Leu Thr | His Ser Ile Phe Asn Ala Glu Leu Tyr |
| 115 | 120 | 125 |
| Ser Pro | Glu Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu | |
| 130 | 135 | 140 |
| Glu Gln | Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly | |
| 145 | 150 | 155 160 |
| Pro Ser | His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys | |
| | 165 | 170 175 |
| Ser Tyr | Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val | |
| | 180 | 185 190 |
| Ile Val | Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His | |
| | 195 | 200 205 |
| Ser Leu | Val Gly Lys His Cys Glu Asp Gly Val Cys Thr Val Thr Ala | |
| 210 | 215 | 220 |
| Gly Pro | Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His | |
| 225 | 230 | 235 240 |
| Val Thr | Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu | |
| | 245 | 250 255 |
| Ala Cys | Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Ser Asp Leu | |
| | 260 | 265 270 |
| Ala Tyr | Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Thr Asp Arg | |
| | 275 | 280 285 |
| Glu Lys | Glu Ile Ile Arg Gln Ala Ala Val Gln Gln Thr Lys Glu Met | |
| 290 | 295 | 300 |
| Asp Leu | Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser | |
| 305 | 310 | 315 320 |
| Thr Gly | Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile | |
| | 325 | 330 335 |
| Tyr Asp | Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met | |
| | 340 | 345 350 |
| Asp Arg | Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu | |
| | 355 | 360 365 |
| Cys Asp | Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu | |
| 370 | 375 | 380 |
| Glu Glu | Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr | |
| 385 | 390 | 395 400 |
| Asp Val | His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys | |
| | 405 | 410 415 |

Asp Val Asn Ile Thr
420

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
50 55 60

Thr Ala Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met
65 70 75 80

Phe His Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val
85 90 95

Phe Gln Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln
100 105 110

Ile Leu Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys
115 120 125

Glu Gly Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn
130 135 140

Lys Lys Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala
145 150 155 160

Lys Val Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His
165 170 175

Ala His Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val
180 185 190

125

Thr Ala Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile
 195 200 205
 Leu His Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met
 210 215 220
 Thr Glu Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro
 225 230 235 240
 Asp Leu Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly
 245 250 255
 Asp Arg Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys
 260 265 270
 Glu Met Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro
 275 280 285
 Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp
 290 295 300
 Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val
 305 310 315 320
 Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr
 325 330 335
 Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr
 340 345 350
 Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser
 355 360 365
 Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys
 370 375 380
 Tyr Lys Asp Ile Asn Ile Thr
 385 390

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Glu | Ile | Thr | Leu | Lys | Asp | Tyr | Ala | Met | Arg | Phe | Gly | Gln | 1 | 5 | 10 | 15 |
| Thr | Lys | Thr | Ala | Lys | Asp | Leu | Gly | Val | Tyr | Gln | Ser | Ala | Ile | Asn | Lys | 20 | 25 | 30 | |
| Ala | Ile | His | Ala | Gly | Arg | Lys | Ile | Phe | Leu | Thr | Ile | Asn | Ala | Asp | Gly | 35 | 40 | 45 | |
| Ser | Val | Tyr | Ala | Glu | Glu | Val | Lys | Pro | Phe | Pro | Ser | Asn | Lys | Lys | Thr | 50 | 55 | 60 | |
| Thr | Ala | Met | Ala | Glu | Asp | Asp | Pro | Tyr | Leu | Gly | Arg | Pro | Glu | Gln | Met | 65 | 70 | 75 | 80 |
| Phe | His | Leu | Asp | Pro | Ser | Leu | Thr | His | Thr | Ile | Phe | Asn | Pro | Glu | Val | 85 | 90 | 95 | |
| Phe | Gln | Pro | Gln | Met | Ala | Leu | Pro | Thr | Ala | Asp | Gly | Pro | Tyr | Leu | Gln | 100 | 105 | 110 | |
| Ile | Leu | Glu | Gln | Pro | Lys | Gln | Arg | Gly | Phe | Arg | Phe | Arg | Tyr | Val | Cys | 115 | 120 | 125 | |
| Glu | Gly | Pro | Ser | His | Gly | Gly | Leu | Pro | Gly | Ala | Ser | Ser | Glu | Lys | Asn | 130 | 135 | 140 | |
| Lys | Lys | Ser | Tyr | Pro | Gln | Val | Lys | Ile | Cys | Asn | Tyr | Val | Gly | Pro | Ala | 145 | 150 | 155 | 160 |
| Lys | Val | Ile | Val | Gln | Leu | Val | Thr | Asn | Gly | Lys | Asn | Ile | His | Leu | His | 165 | 170 | 175 | |
| Ala | His | Ser | Leu | Val | Gly | Lys | His | Cys | Glu | Asp | Gly | Ile | Cys | Thr | Val | 180 | 185 | 190 | |
| Thr | Ala | Gly | Pro | Glu | Asp | Cys | Val | His | Gly | Phe | Ala | Asn | Leu | Gly | Ile | 195 | 200 | 205 | |
| Leu | His | Val | Thr | Lys | Lys | Lys | Val | Phe | Glu | Thr | Leu | Glu | Ala | Arg | Met | 210 | 215 | 220 | |
| Thr | Glu | Ala | Cys | Ile | Arg | Gly | Tyr | Asn | Pro | Gly | Leu | Leu | Val | His | Pro | 225 | 230 | 235 | 240 |
| Asp | Leu | Ala | Tyr | Leu | Gln | Ala | Glu | Gly | Gly | Gly | Asp | Arg | Gln | Leu | Gly | 245 | 250 | 255 | |
| Asp | Arg | Glu | Lys | Glu | Leu | Ile | Arg | Gln | Ala | Ala | Leu | Gln | Gln | Thr | Lys | 260 | 265 | 270 | |
| Glu | Met | Asp | Leu | Ser | Val | Val | Arg | Leu | Met | Phe | Thr | Ala | Phe | Leu | Pro | 275 | 280 | 285 | |

127

Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp
 290 295 300
 Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val
 305 310 315 320
 Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr
 325 330 335
 Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr
 340 345 350
 Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser
 355 360 365
 Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys
 370 375 380
 Tyr Lys Asp Ile Asn Ile Thr
 385 390

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 1 5 10 15
 Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60
 Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys
 65 70 75 80
 Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr
 85 90 95

128

Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe
 100 105 110

Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu
 115 120 125

Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys
 130 135 140

Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His
 145 150 155 160

Ile Lys Thr His Gln Asn Lys Lys Gly Gly Pro Gly Val Ala Leu Ser
 165 170 175

Val Gly Thr Leu Pro Leu Asp Ser Gly Ala Gly Ser Glu Gly Ser Gly
 180 185 190

Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr Asn Met Val Ala Met Glu
 195 200 205

Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu Ala Asn Ser Gly Ile Asn
 210 215 220

Val Met Gln Val Ala Asp Leu Gln Ser Ile Asn Ile Ser Gly Asn Gly
 225 230 235 240

Phe

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGGAMTNYCC

10

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30
His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45
Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala His Gln Asn Ser Gln Thr
50 55 60
His Gln Ala Ser Leu Ser Lys Gln
65 70